In the claims:

Please amend claims as follows:

-- 1. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (5)~~:

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of the ~~sequence pairs~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~74~~)~~, SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~78~~)~~, SEQ IDS NOS: ~~(~~72~~)~~ and ~~(~~71~~)~~, SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~74~~)~~, ~~and~~ SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~78~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) isolating said DNA fragment;

(4) determining the nucleotide sequence of said DNA fragment; and

(5) ~~identifying the microorganism by~~ comparing the sequence of the amplified *gyrB* gene DNA fragment to known *gyrB* gene DNA fragment sequences.

2. (Currently Amended) The method for identifying a microorganism according to claim 1, wherein the amino acid sequence pairs that are used are ~~sequence pairs~~ SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~74~~)~~, SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~78~~)~~, SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~74~~)~~, or SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~78~~)~~; and said microorganism belongs to *proteobacteria*.

3. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (8)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~71~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~73~~)~~;

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid~~

~~sequences~~SEQ ID NOS: ~~(~~70~~)~~ and ~~(~~71~~)~~;

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

4. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (8)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~74~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~73~~)~~;

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~70~~)~~ and ~~(~~74~~)~~;

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

5. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (8)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~74~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to

produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~73~~)~~;

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~70~~)~~ and ~~(~~74~~)~~;

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

6. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~73~~)~~;

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: ~~(~~76~~)~~ and ~~(~~71~~)~~, SEQ ID NOS: ~~(~~76~~)~~ and ~~(~~74~~)~~, or SEQ ID NOS: ~~(~~76~~)~~ and ~~(~~75~~)~~;

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

7. (Currently Amended) A method for identifying a microorganism, comprising ~~the following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~77~~)~~;

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: ~~(79)~~ and ~~(71)~~, SEQ ID NOS: ~~(79)~~ and ~~(74)~~, or SEQ ID NOS: ~~(79)~~ and ~~(75)~~;

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

8. (Currently Amended) A method for identifying a microorganism, comprising the following steps (1) to (6):

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(69)~~ and ~~(77)~~;

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: ~~(80)~~ and ~~(71)~~, SEQ ID NOS ~~(80)~~ and ~~(74)~~, or SEQ ID NOS: ~~(80)~~ and ~~(75)~~;

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~identifying the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

9. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (5)~~:

(1) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of ~~the sequence pairs~~SEQ ID NOS: ~~(69)~~ and ~~(74)~~, SEQ ID NOS: ~~(69)~~ and ~~(78)~~, SEQ ID NOS: ~~(72)~~ and ~~(71)~~, SEQ ID NOS: ~~(72)~~ and ~~(74)~~, ~~and~~ SEQ ID NOS ~~(72)~~ and ~~(78)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) isolating said DNA fragment;

(4) determining the nucleotide sequence of said DNA fragment; and

(5) ~~detecting the microorganism by~~ comparing the nucleotide sequence of said amplified *gyrB* gene DNA fragment to known *gyrB* gene DNA fragment sequences.

10. (Currently Amended) The method for detecting a microorganism according to claim 9, wherein the amino acid sequence pairs that are used are ~~sequence pairs~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~74~~)~~, SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~78~~)~~, SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~74~~)~~, or SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~78~~)~~; and said microorganism belongs to *proteobacteria*.

11. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (8)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~71~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~73~~)~~;

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~70~~)~~ and ~~(~~71~~)~~;

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two primers to produce two *gyrB* gene DNA fragments;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

12. (Currently Amended) A method for detecting a microorganism, comprising ~~the~~

~~following steps (1) to (8)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~74~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~73~~)~~;

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~70~~)~~ and ~~(~~74~~)~~;

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

13. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (8)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~74~~)~~;

(2) amplifying *gyrB* gene DNA from the microorganism using said two primers to produce a *gyrB* gene DNA fragment;

(3) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~73~~)~~;

(4) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~70~~)~~ and ~~(~~74~~)~~;

(5) amplifying the *gyrB* gene DNA fragment produced in step (2) using said two pairs of primers, so that two *gyrB* gene DNA fragments are produced;

(6) isolating said two DNA fragments;

(7) determining the nucleotide sequences of said two DNA fragments; and

(8) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

14. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~72~~)~~ and ~~(~~73~~)~~;

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: ~~(~~76~~)~~ and ~~(~~71~~)~~, SEQ ID NOS: ~~(~~76~~)~~ and ~~(~~74~~)~~, or SEQ ID NOS: ~~(~~76~~)~~ and ~~(~~75~~)~~;

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

15. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~ SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~77~~)~~;

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: ~~(~~79~~)~~ and ~~(~~71~~)~~, SEQ ID NOS: ~~(~~79~~)~~ and ~~(~~74~~)~~, or SEQ ID NOS: ~~(~~79~~)~~ and ~~(~~75~~)~~;

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences.

16. (Currently Amended) A method for detecting a microorganism, comprising ~~the following steps (1) to (6)~~:

(1) synthesizing forward and reverse primers based on a single pair of ~~amino acid sequences~~SEQ ID NOS: ~~(~~69~~)~~ and ~~(~~77~~)~~;

(2) synthesizing forward and reverse primers based on a single pair of amino acid sequences selected from the group consisting of SEQ ID NOS: ~~(~~80~~)~~ and ~~(~~71~~)~~, SEQ ID NOS: ~~(~~80~~)~~ and ~~(~~74~~)~~, or SEQ ID NOS: ~~(~~80~~)~~ and ~~(~~75~~)~~;

(3) amplifying *gyrB* gene DNA from the microorganism using said two pairs of primers to produce two *gyrB* gene DNA fragments;

(4) isolating said two DNA fragments;

(5) determining the nucleotide sequences of said two DNA fragments; and

(6) ~~detecting the microorganism by~~ comparing the sequences of said two *gyrB* gene DNA fragments to known *gyrB* gene DNA fragment sequences. --